

## SEQUENCE LISTING

<110> Power, Christine  
Lavrovsky, Yan

<120> Treatment of Fibrotic Disease

<130> ARS.122

<140> US 10/570,122

<141> 2006-02-28

<150> EP 03102723.8

<151> 2003-09-08

<160> 20

<170> PatentIn version 3.1

<210> 1

<211> 492

<212> DNA

<213> Homo sapiens

<400> 1

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gagtggctcc gacgggagct gcgggagatg caggcgcagg acaggcagct ggcagggcag      300
ctgctgcggc tcggggccca gctgcaccga ctgaagatgg accaagcctg tcacctgcac      360
caggagctgc tggatgaggc cgagctggag ctggagctgg agcccggggc cggcctagcc      420
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<213> Homo sapiens

<400> 2

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 Lys Leu Gln Leu Gln Thr Arg Arg Pro Ser Tyr Leu Glu Trp Thr Ala  
                   35                  40                  45  
 Gln Val Gln Ser Gln Ala Trp Arg Arg Ala Gln Ala Lys Pro Gly Pro  
                   50                  55                  60  
 Gly Gly Pro Gly Asp Ile Cys Gly Phe Asp Ser Met Asp Ser Ala Leu  
 65                  70                  75                  80  
 Glu Trp Leu Arg Arg Glu Leu Arg Glu Met Gln Ala Gln Asp Arg Gln  
                   85                  90                  95  
 Leu Ala Gly Gln Leu Leu Arg Leu Arg Ala Gln Leu His Arg Leu Lys  
                   100                  105                  110  
 Met Asp Gln Ala Cys His Leu His Gln Glu Leu Leu Asp Glu Ala Glu  
                   115                  120                  125  
 Leu Glu Leu Glu Leu Glu Pro Gly Ala Gly Leu Ala Leu Ala Pro Leu  
                   130                  135                  140  
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 145                  150                  155                  160  
 Thr Leu Cys

<210> 3  
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Met Ser Leu Gly Leu Leu Lys Phe Gln Ala Val Gly Glu Glu Asp Glu  
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 Glu Asp Glu Glu Gly Glu Ser Leu Asp Ser Val Lys Ala Leu Thr Ala  
                   20                  25                  30  
 Lys Leu Gln Leu Gln Thr Arg Arg Pro Ser Tyr Leu Glu Trp Thr Ala  
                   35                  40                  45  
 Gln Val Gln Ser Gln Ala Trp Arg Arg Ala Gln Ala Lys Pro Gly Pro  
                   50                  55                  60  
 Gly Gly Pro Gly Asp Ile Cys Gly Phe Asp Ser Met Asp Ser Ala Leu  
 65                  70                  75                  80  
 Glu Trp Leu Arg Arg Glu Leu Arg Glu Met Gln Ala Gln Asp Arg Gln  
                   85                  90                  95

Leu Ala Gly Gln Leu Leu Arg Leu Arg Ala Gln Leu His Arg Leu Lys  
                   100                  105                  110  
 Met Asp Gln Ala Cys His Leu His Gln Glu Leu Leu Asp Glu Ala Glu  
                   115                  120                  125  
 Leu Glu Leu Glu Leu Glu Pro Gly Ala Gly Leu Ala Leu Ala Pro Leu  
                   130                  135                  140  
 Leu Arg His Leu Gly Leu Thr Arg Met Asn Ile Ser Ala Arg Arg Phe  
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 gcctgtcacc tgcaccagga gctgctggat gaggccgagc tggagctgga gctggagccc 180  
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                   20                  25                  30  
 Leu His Arg Leu Lys Met Asp Gln Ala Cys His Leu His Gln Glu Leu  
                   35                  40                  45  
 Leu Asp Glu Ala Glu Leu Glu Leu Glu Leu Glu Pro Gly Ala Gly Leu  
                   50                  55                  60  
 Ala Leu Ala Pro Leu Leu Arg His Leu Gly Leu Thr Arg Met Asn Ile  
 65                  70                  75                  80

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20 25 30

Leu His Arg Leu Lys Met Asp Gln Ala Cys His Leu His Gln Glu Leu  
35 40 45

Leu Asp Glu Ala Glu Leu Glu Leu Glu Leu Glu Pro Gly Ala Gly Leu  
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Ala Leu Ala Pro Leu Leu Arg His Leu Gly Leu Thr Arg Met Asn Ile  
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Ser Ala Arg Arg Phe Thr Leu Cys His His His His His His  
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20 25 30

Leu His Arg Leu Lys Met Asp Gln Ala Cys His Leu His Gln Glu Leu  
35 40 45

Leu Asp Glu Ala Glu Leu Glu Leu Glu Leu Glu Pro Gly Ala Gly Leu  
50 55 60

Ala Leu Ala Pro Leu Leu Arg His Leu Gly Leu Thr Arg Met Asn Ile  
65 70 75 80

Ser Ala Arg Arg Phe Thr Leu Cys  
85

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<400> 8

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1          5          10          15

Ala Gln Asp Arg Gln Leu Ala Gly Gln Leu Leu Arg Leu Arg Ala Gln
          20          25          30

Leu His Arg Leu Lys Met Asp Gln Ala Cys His Leu His Gln Glu Leu
          35          40          45

Leu Asp Glu Ala Glu Leu Glu Leu Glu Leu Glu Pro Gly Ala Gly Leu
          50          55          60

Ala Leu Ala Pro Leu Leu Arg His Leu Gly Leu Thr Arg Met Asn Ile
65          70          75          80

Ser Ala Arg Arg Phe Thr Leu Cys His His His His His His
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<210> 9  
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gagctggagc tggagcccgg ggccggccta gccctggccc cgctgctgcg gcacctgggc      180
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Ala Gln Leu His Arg Leu Lys Met Asp Gln Ala Cys His Leu His Gln
          20          25          30

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Glu Leu Leu Asp Glu Ala Glu Leu Glu Leu Glu Leu Glu Pro Gly Ala  
                   35                                  40                                  45

Gly Leu Ala Leu Ala Pro Leu Leu Arg His Leu Gly Leu Thr Arg Met  
           50                                  55                                  60

Asn Ile Ser Ala Arg Arg Phe Thr Leu Cys  
   65                                  70

<210> 11  
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<400> 11

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Ala Gln Leu His Arg Leu Lys Met Asp Gln Ala Cys His Leu His Gln  
                   20                                  25                                  30

Glu Leu Leu Asp Glu Ala Glu Leu Glu Leu Glu Leu Glu Pro Gly Ala  
                   35                                  40                                  45

Gly Leu Ala Leu Ala Pro Leu Leu Arg His Leu Gly Leu Thr Arg Met  
           50                                  55                                  60

Asn Ile Ser Ala Arg Arg Phe Thr Leu Cys His His His His His His  
   65                                  70                                  75                                  80

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